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humPMS2 (2574) 2661 CATTCTCAGAAC-----2730
AtPMS2 (2267) CTTTACTCACTTTACCTGATGACGACAATGTCAATGATGATGATGATGATGATGCAACCATCTCATTGGC
Consensus (2661) C TT CTCA A
humPMS2 (2587) ----
AtPMS2 (2337) ATGA
Consensus (2731)

```

Figure 1. Alignment between human PMS2 (humPMS134) and Arabidopsis thaliana homologue of PMS2 (AtPMS2) DNA sequences. Similarity is 48.1%; identity is 48.1%. Black boxes show identical nucleotides.

1 70

humPMS2 (1) --MERAEESSTEPAKATKEFDKSVHQICSGQVVLSSAVKELVENS LDAGATNIDLKLKQYGVLLIEV

AtPMS2 (1) MQGDSSPPTITSSPLIRPINENVRICSGQVILDLSSAVKELVENS LDAGATNIEINLRDYGEYFQV

Consensus (1) D A S S T A IKPI R IH ICSGQVIL LSSAVKELVENS LDAGAT IDI LKDYG D V

71 140

humPMS2 (69) SDNGCCVEEENF-----EGTILFHTSKIQEFADLTQVETFGFRGEALSSSLCALSDVTISCHA

AtPMS2 (71) IDNGCCISPTNFKVCVQILRRTFDVLALFHTSKLEDFIDILNLTIVGFRGEALSSSLCALGNLTVEIRTK

Consensus (71) DNGCGI NF D L LKHHTSKI DF DL NL TFGFRGEALSSSLCAL LTI T

141 210

humPMS2 (128) SAKVGTREMFHDHNGKI IQKTPYPRPGTTVSVOQLFSTLPVRRKEFORNIKEYAKMVOVLHAYCI-SAG

AtPMS2 (141) NEPVATLTFDHSGLLTABKKTARQIGTTITURKLFSLNLPVRSKEFKENIRKEYCKLNSLLNAYALAKG

Consensus (141) VAT L FDH G I R GTTVSV LFS LPVR KEF RNIKEYAKLV LL AY IIA G

211 280

humPMS2 (198) IRVSGTNOLCGQKRPVVTCTGSPSKEE--GSVFGQKQLQSLIFVQLPPSDSVCEEYGLSCSDALHNL

AtPMS2 (211) VRFVCSNITTEKNPKSVVLNTOGRGSLKDIITVFGISTFTSQQ-----

Consensus (211) IR CSN G K VL T G STKDNISVFG SL P

281 350

humPMS2 (268) YISGFISQCTHGVGRSSTDRQFFFINRRCDPAKVCRLVNEVHEMYNRHOYFFVVLNISVDSECVINVT

AtPMS2 (255) ---G-----TGNLADRCVFFINGREVEMKVKSLVNELKDTSSRKYPVTILDFIVPGGACILNVT

Consensus (281) G GR DRQFFFIN RP D KV KLVNELY YP IL V DINVT

351 420

humPMS2 (338) PDKKQIILLQEKLLLAVALKTSLIGMFDSDVNKLNVSQPLLDVEGNLIKMAADLEKPMVEKQDQSPSLR

AtPMS2 (314) PDKRKVFPSDET-----SV-----

Consensus (351) PDKR I DE

421 490

humPMS2 (408) TGEKKDVSISRLEAFSLRHTTENKPHSPKTPPPRRSPILGQKRGMLSSSTSGAISDKGVLRPQKEAVSS

AtPMS2 (328) -----TGSRLREGLNEIYSSSNASYIVNRFENSEQPDKAGVSSFQKKSNNLLSEGIVLDVSSKTRILG

Consensus (421) I LREA HSS N H E S ISD VL

491 560

humPMS2 (478) SHGPSDPTDRAEVEKDSGHGSTSVDSSEGFSPIDTGSCHSSEYAASSPCDRGSQEHVDSQEKAPETDSFS

AtPMS2 (389) EAIEKENPSLREVEIDNSSPMEKFKFEIKACGTKKGEGLSVHDVTHLDKTPSKGLPQLNVTEKVTASK

Consensus (491) D EVE D E A S S DK L DA

561 630

humPMS2 (548) DVDCHSNQEDTGCKRVLVLPQPNLATPNTIRFKKEBELSSSDICQKLVNTQDMSASQVDVAVKINKKVP

AtPMS2 (459) DLSSRSS-----EAQSTLNTFVTMGKRHENISTILSETPVLNRQTSSYRVEKSKFVRALASRCLE

Consensus (561) DL S F T L K ILS S I S M S DV K LV

631 700

humPMS2 (618) LDFSMSSSLAKRIKQLHHEAQOSECEQNYRKFRKICPGENQAAEDELRLKEISKTMFAEMEIIQQFNLGFI

AtPMS2 (522) GDQLDDMVISKEDMTPSERDSELGNRISPTQA-----D-----NVERHERVILGQFNLGFI

Consensus (631) D L K E G A M IIGQFNLGFI

701 770

humPMS2 (688) ITKLNEEDIFIVDQHAIDERYNFEMIQHVLQGORLIAPQTLNITAVNEAVLIENLEIRKNGFDVVIDE

AtPMS2 (573) IAKIERDIFIVDQHAADKFNFEHLARSVLNQCPQLQPLNLEISPEBEVTVLMHMDITENGFLLEENP

Consensus (701) I KL DIFIVDQHA DEKFNFE L TVLN Q LI P L LS E LI LDI R NGF

771 840

humPMS2 (758) NAEVTERAKIISLETSKNWTFFGQDVDELTFMSDSPGVMC-----PSRVKQMEASRACK

AtPMS2 (643) SAPPGKHFRRAIDYSKNITFGVEDLKDISTGDNHGECSVASSYKTSKTDSTICPSRVKRAMLASRACS

Consensus (771) AP KL AIP SKN TFG DL DLI L D G PSRVK M ASRACR

841 907

humPMS2 (815) SVMIGTALNTSEMKKLITMGEMDHPWNCPHGRPTMRHIANGVISQN-----

AtPMS2 (713) SVMIGDPARKNEMQKIVEHLADLES PWNCPHGRPTMRHLVDITTLTLTPDDDNVNDDDDDATISLA

Consensus (841) SVMIG L EM KII HLADLD PWNCPHGRPTMRHI L I

Figure 2. Alignment between human PMS2 (humPMS134) and Arabidopsis thaliana homologue of PMS2 (AtPMS2) amino acid sequences. Similarity is 41.5%; identity is 31.1%. Black boxes show identical residues.

1 70

humPMS2 (1) -----MERAESS-----EPAKAIKPIDRKSWHOCSECVLSLSTAVKELVENSLEAGATNIDL

AtMLH1 (1) MIDDSSLTABMEEBESPATTIVPREPKIQRLEESVNNRIAAEIIQRPVSAVKELVENSLEADSSISV

Consensus (1) ME ES AT I ID V I AG VI SAVKELVENSLEA AS I L

71 140

humPMS2 (57) KLKHYGVDLIEVSDNGCCVEEENFEGLTLKHTSKIQEFADLTQVETFGFRGEALSSLCALSDVISTCH

AtMLH1 (71) VVKDGGLKLIQVSDDGHGIRREDLPILCERHTTSKLTKEFDLFSLSMGERGEALASMTYVAHVVTITIT

Consensus (71) LKD GL LI VSD G GI E L KH TSKI F DL L S GFRGEALASL LA VTIST

141 210

humPMS2 (127) ASAKVETLMFDHNGKIIQKTPYPRPGTIVSVOQLFSTLPVHEEFGRNIKKENAKMNOVHAYCHISA

AtMLH1 (141) KGQIHGYEVSRYDGVMEHEPKACAAGKGTQIMVENLEYNMIARRETLQNSADDYGRINDLSRMATHYN

Consensus (141) G RL F KGT I V NLF L R K Q N DYAKIV LL I

211 280

humPMS2 (197) GIRVSCINQLGQKRPVICTGGSPSIKENIGSVFGQKQLQSLIPFVQLPPSDSVCEEYGLSCSALHNL

AtMLH1 (210) NVSHSCRKH---CAVKADVHSVVSFSPRLDSIRSVYGVSVAKNLM---KV---E-----VSSCSGGCT

Consensus (211) I SC G V S SPS D I SVFG LI L LS DA

281 350

humPMS2 (267) FYISCFISQTHGVGRSSTDRQFFFINRPCDPAKVCLVNEVSHM-YNRHQYPFVVLNHSVDSECVGIN

AtMLH1 (264) EDMECFISNSNYVAKKTIL---VLFINDRLVECSALKKAIEIVAAATLPKASKPFVYMSINLPREHVDIN

Consensus (281) F I GFISN H KS FIN R D A L R I VY K PFV L I L E VGIN

351 420

humPMS2 (336) VTFFKQIILLQEEKLLAVLKTSLIGMFDSVKNLNVSQPLLDEVEGNLIIMHADLEKPMVFKQDQSPS

AtMLH1 (331) IHTFKKEVSLNQEIIEIMIQ-----SEVE-----VILRNENDTRTFQKQVEYIQ

Consensus (351) I P KK I L III MI S IKL A K E

421 490

humPMS2 (406) LRTGEEKQDVSIIRLREAFSLRHTTENKPHSPKTPPEPRRSILQKRGMLSSSTSGAISDKGVLRPQKEAV

AtMLH1 (377) STLTSCQSDSPVSKPSG---QKQKQVNVNKMVRTDSSDAARLHAFLQPKPQSLPDKVSSLSVVRSSV

Consensus (421) K D IS A T P P G A L L K AV

491 560

humPMS2 (476) SSSHGSDPTIRAEVEKDSGHGSTVDSEGSFIPDTGSHCSSEYAASSPGDRGSCHEHVDSEKAPETDS

AtMLH1 (443) RQRNPKETALSSVQE-----LIA--G-----V-DSCHPCMLETVRNCTYVGMADDV

Consensus (491) P D D A V I S G E V DD

561 630

humPMS2 (546) FSDVDCHSNQEDTGCKFRVLPOPTNLATPNTKRFKKEEILSSSDICQKLVNTQDMSASQVDVAVKINKKV

AtMLH1 (489) FALVQYN---THLYLAN-----VVNLSEKLMYQOTLRRFAHFNAIQLSDPAPLSELILLALKEEDL

Consensus (561) FA V T SK L N I S S L L L

631 700

humPMS2 (616) VPLDFSMSSIAKRILKQLHHEAQOSEGEQNYRKRRAKICPGENQAEDELRKEISKTFPAEMIIIGQFNLG

AtMLH1 (547) DEGNDTKDDIKERIAEMNTELLKEKAEMLEBYSVHIDSSANLSRLPVILDQYTPDMVRVPEFL--LCLG

Consensus (631) P S L RI L E AE F I NA I S M E I LG

701 770

humPMS2 (686) FIITKLNIIDIFIVDQHATDEKYNFEMLQOHTVLQQRLLIAPOTLNLTAVNEAVLIENLEIFRKNGFVFI

AtMLH1 (615) NDVEWEDKSCFQGVSSAIGNFYAMHPPLLPNPSCDGIQFYSKRGESSQEKSDIEGNVDMEDNLDQILLS

Consensus (701) I E A F G I SA A L NLDI D L

771 840

humPMS2 (756) ENAPVTERAKLISLPTSKNVTFGPDVDDELIFMLSDSPGVMCRPSRIVKQMFASRACRKSVMITALNTS

AtMLH1 (685) EAENAWAQR-----EWSIQHVLFPMSRLFLKPPFASMASNGTFVKVASLEKLYKIFERC-----

Consensus (771) D R WS L L M S VK K K

841 877

humPMS2 (826) EMKKLITHMGEMDHPWNCPHGRPTMRHIANLGVISQN

AtMLH1 (738) -----

Consensus (841) -----

Figure 3. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS2 homologue MLH1 (AtMLH1) amino acid sequences. Similarity is 30%; identity is 18.4%. Black boxes show identical residues.

00249601.13300

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1                               70
humPMS2 (1) MERAESSSTEPAKAIKIDRKSVMQICSGQVVLSTLSTAKELVENSIDAGATNIDLKLDYGVDLIEVSD
AtPMS1 (1) -----MKLIKALPEGVRISMREGIIMFDMARVVELVFNLSIDAGATKVSIFVGVVSCS-VKIVD
Consensus (1) K IKPI H I SG IM LA V ELV NSLDAGAT I I L I V D

71                               140
humPMS2 (71) NGCGVEENFEGTLTKHHTSKIQEADL-EGVETFGFRGEALSSLCALSDVTIS-CHASAKVGTILMFDH
AtPMS1 (59) DSCGVSRDDLVLGERYATSKFHD-TNVEIASETFGFRGEALASISDISLLEVRKAIGRPNCYKVMKG
Consensus (71) G GV D L KH TSK DF L T ETFGFRGEALASI IS L I T G R M

141                               210
humPMS2 (140) NGKIIQKTPYFRP-RGTTVSVQQLFSTLPVRHKEFQRNIIKKEYAKMVQVLHAYCIIISAGI-----
AtPMS1 (129) SKCLHLGIDDDRKDSGTTVTVRDLHYSGPVRKRYMSSPKKVLSEIKKCVFRIALVHSNVFSVLDIESD
Consensus (141) I R GTTVSV LF S PVR K Q KK I L II A I

211                               280
humPMS2 (199) -----RVSCTNQLGQGRQPVVCTGGSPSIKENISV
AtPMS1 (199) EELFQTNPSSSAFSLMRDAGTEAVNSLCKVNVTDGMLNVSGFECADDWPTDQQTGRNRNLOSNSPYI
Consensus (211) VS K TG I N G I

281                               350
humPMS2 (231) -----FGQKQLQSLIFVQLPISDSVCEYGLSCSDALHNFYISCFISQCTHGVGRSSTDRQF
AtPMS1 (269) LCIIACPRRLYESEFESKTHVEFKWGVLAFTIRITLANWKKDRIELPDCGADILAKDRQDLIEDKI
Consensus (281) F S I F P A E LA L G G D

351                               420
humPMS2 (290) FFINR-----RPCDPAKVCLRVNEVYHMYNRHQYEFVVLNLSVSECVDINVTDPKRRQILL
AtPMS1 (339) RLQNGSLFSILHFLDADWPEAMEPAKKLKRSDHAPCSSLFPASADFKQDGYFSPRKDWNSPECEVEI
Consensus (351) N DPAK H FP D V I L

421                               490
humPMS2 (346) QEEKLLLAVALKTSLIGMFDSDOVNKLNVSCPLLEVEGNLIKMHAADEKPMVEKIDQSPSLRTGEEKKDV
AtPMS1 (409) KIQNPKEQGTVAGFESRIDSLLQSRDIEMTINEDFPQVTDLLLETSLVADSKCRFLTRCQIITPVNINH
Consensus (421) DS LN I Q D L A L KQ S T

491                               560
humPMS2 (416) SISRLREAFS-----LRHTTENKPHSEKTEPRRSPLGQ
AtPMS1 (479) DFMKDSVLNLFQFQGLKDELVDVSNICGKHLRGCSRVSLTFHEBPKSEVEGYESVVMILENEKQSSPRV
Consensus (491) K D L H P P K S

561                               630
humPMS2 (450) KRGMLSSTSGAISDKGVLRPQKEAVSSSHG--ISDPTDRAEVEKDSGHGSTSVSEGESIPDTGSHCSS
AtPMS1 (549) LETREGGCSYCDVYSRTPDCSLGSSWQDQTDWFTQCSSDRGCGVIGEDFNIPISTABEDSYDEKVGSKK
Consensus (561) S SDK A S P SDRA V T IDS F D

631                               700
humPMS2 (518) EYAASSPDRGSQEHVDSCF-----KAFETDDSFSDVDCHSNQEDTGCKFRVLEOPTNLATPNTKRFKKE
AtPMS1 (619) YLSSVNVGSSVTGSCFCLSEWSPMYSTGATKWESEYQKGRILEQSLRLGRMEDPEFCFSAANNIKFDH
Consensus (631) AA G S S E P SD D K LP P S

701                               770
humPMS2 (583) EILSSSLQCKLVNTQDMSASQVDVVKANKK---VVPLDFSMSSLAIRIKQLHHEAQSECEENYRK
AtPMS1 (689) EVIPEMCCETGTDSFTAIONCTQLADKCKSSWGHADDVRIDQYSIRKEKFSYMDGTNNASKRSKRS
Consensus (701) EII D C S LA KI K L SI K QN G Q KK

771                               840
humPMS2 (649) RAKICPGENQ-----
AtPMS1 (759) RSAPPFYREKKRIFSLCKSDTKPKNSDPSEPDLECLTQPCNASQMHLCISILDVSYDHIQETEKRLS
Consensus (771) RA

841                               910
humPMS2 (659) -----
AtPMS1 (829) SASDLKASAGCRTVHSEQDEVDHEDFSSEEFDPKSTTKWRHNCAVSQVPKESHELHGQDGVFDISSG
Consensus (841)

911                               980
humPMS2 (659) -----AADELRLKEISKTMFAEMEIIIGFNLGFIITKLNEIFIVDQHADEKYNFEMIQOHTVLQGGRL
AtPMS1 (899) LLHLRSDSLVPESINRHSLEDAKVLCQVDKKYPIVACGTVAIVDQHAADERIRLEELRTKFINDEALLI
Consensus (911) A E L I K D II Q FI I IV DQHA DEK E L I A I

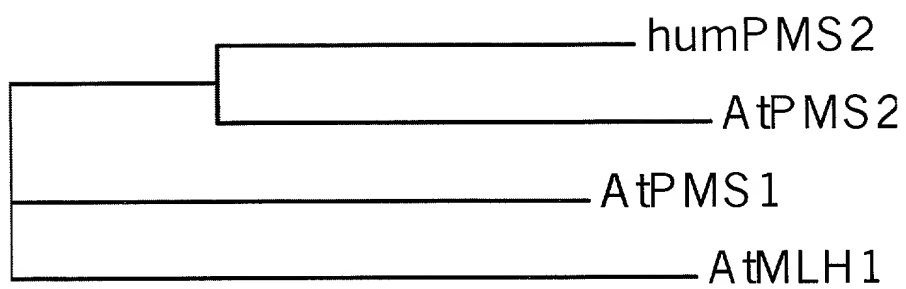
981                               1050
humPMS2 (724) IAPQTLNTAVNEAVIENLEIFRKNSEDFVIDENAPVTERAK-----ISLPTSKNWTFGPQ
AtPMS1 (969) FVLTLKVIPEMGYQLQSYSEQIRDWGICNITVEGSTSFKKNMSIIQRKPTPITNAVECILGVNLSDV
Consensus (981) L M LL E R GF I A S K L ALP

1051                               1120
humPMS2 (782) DVDELIFMLSDSPGVMCRPSRVKQMFASRACRKSVMITGTAINTSEMKKLITHMGEMDHPWNGHGRPTMR
AtPMS1 (1039) DLLFLQQLADTDGSSTIIPSVLRVLNSKACRGAIMFQDSLLPSCSLIIDGLKQTSLSLFCQAHGRPTTV
Consensus (1051) DL E I LADS G P V M SKACR AIM G AL SE II L FNC HGRPT

1121                               1164
humPMS2 (852) HIANGVISON-----
AtPMS1 (1109) PLVDLAKLHKQIAKLSGRQVWHGLQRREITLDRAKSRLDNAKS-
Consensus (1121) I L I N

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Figure 4. Alignment between human PMS2 (humPMS2) and Arabidopsis thaliana PMS2 homologue PMS1 (AtPMS1) amino acid sequences. Similarity is 24.4%; identity is 15%. Black boxes show identical residues.



**Figure 5.** Phylogenetic tree of the *Arabidopsis thaliana* *PMS2* gene homologues.

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humPMS134 (1) ATGGGCGAGCTGAGAGCTCGAGTACAGAACCTGCTAAGGCG-----ATCAAACCTATTGTCGGAAGT
AtPMS134 (1) ATGCGACGACATTCTTCTCCGCTCCGAGCACTACTAGCTCTCCTTTGATAAGACCTATAAACAGAAACG
Consensus (1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA
71 140
humPMS134 (65) CAGTCCATCAGATTGCTCTGGGCGAGTGGTACTGAGTCTAAGCACTGGCGTAAAGGAGTTAGTAGAAAA
AtPMS134 (71) TAATTACAGAATCTGTTCCGCTCAAGTCACTAGACCTCTCTTCCGCCCTCAAGGAGCTTCTCCAGAA
Consensus (71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA
141 210
humPMS134 (135) CAGTCCGATGCTGGTGGCACTATATATTGATCTAAAGCTTAAGGACTATGGAGTGGATCTTATTGAGATT
AtPMS134 (141) TAGTCCGACGCCGGCGCCAGCAGTATAGAGATTAACTCCGAGACTACGCCCAAGACTATTCTCCAGCTC
Consensus (141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT
211 280
humPMS134 (205) TCAGACAATGGAATGTGGGT-----AGAAGAAG-----AAAACTTCCAAGG-CTTAA-
AtPMS134 (211) ATTTACAATGCTTGTGGCATTTCCCAACCAATTTCAAGGTTTGTGTCCAATTTCCGAAGAACCTTTTG
Consensus (211) GACAATGG TGTGG T A AAG AA CT CGAAG CTT
281 350
humPMS134 (251) -----CTCTGAAACATCAACATCTAAGATTCAAGACTTGCCGACCTAACCAAGTTGAA-ACCT
AtPMS134 (281) ATGTTCTTGCATTTAAGCATCATACTCTAAATAGAGGATTCACAGATCTTTCAATTTGACTACTT
Consensus (281) C CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT
351 420
humPMS134 (311) TTGGCTTTCCGGCGGAAGCTCTGAGCTCACTTTGTGCACTGAGCGATCTCAGCAATTCTACCTG--CCAC
AtPMS134 (350) ATGGCTTTAGAGGAGGAAGCTTGAGCTCTCTGTGTCATTGGGAAATCTCACTGCGGAACAAAGAACAA
Consensus (351) TGG TTT G GG GAAGC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A
421 444
humPMS134 (379) CCATCGCGGAGGTTGGAAGT---
AtPMS134 (420) CAATGAGGCA--GTGCTACGCTC
Consensus (421) G AT GC A GTTG AC

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**Figure 6.** Alignment between human PMS134 (humPMS134) and Arabidopsis thaliana homologue of PMS134 (AtPMS134) DNA sequences. Similarity is 53.2%; identity is 53.2%. Black boxes show identical nucleotides.

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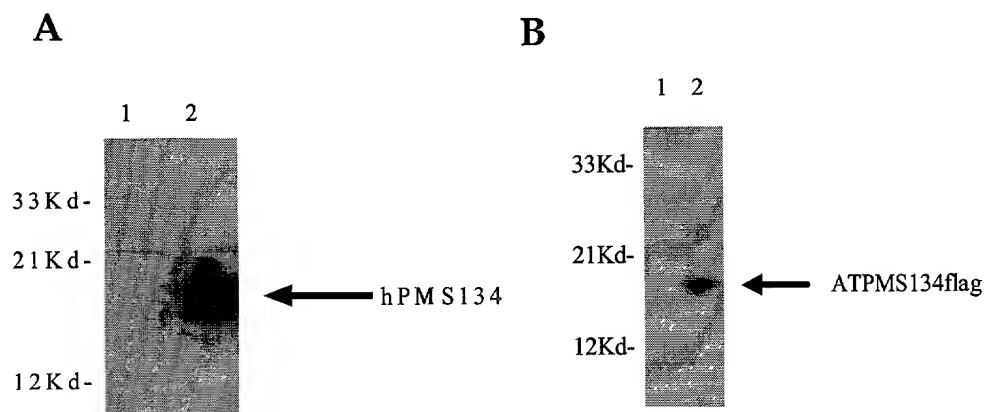
1                                     70
humPMS134 (1) --MERARSSSEPAKAKKPIIDKSVHICSGQVLSLSTAVKELVENS LDAGATNIDLKLKDYGVLLIEV
AtPMS134 (1) MQGDSSPSPTTSSPLIRPNNVNIHICSGQVILDLSSAVKELVENS LDAGATSI EINI RDYGEYFQV
Consensus (1) D A S ST A IKPI R IH ICSGQVIL LSSAVKELVENS LDAGAT IDI LKDYG D V

71                                     140
humPMS134 (69) SDNGCGVEEENF-----ECITLKHHTSKIQEADLTQVEFFRGEALSSLCALSDVTISTCHA
AtPMS134 (71) IDNGCGISPTNFKVCVQILRRTFDVI ALKHHTSKLEDFTDLLNLTFGRGEALSSLCALGNLVEIRTK
Consensus (71) DNGCGI NF D L LKHHTSKI DF DL NL TFGFRGEALSSLCAL LTI T

141
humPMS134 (128) SAKVGT
AtPMS134 (141) NEPVAT
Consensus (141) VAT

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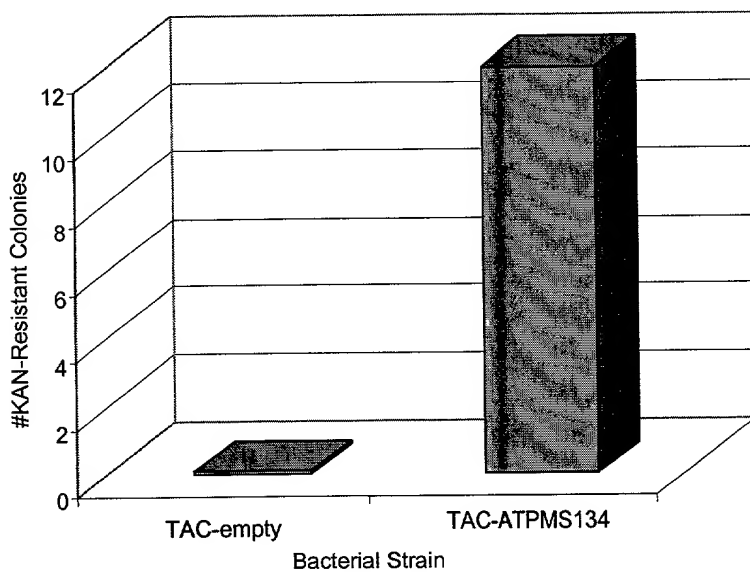
**Figure 7.** Alignment between human PMS134 (humPMS134) and *Arabidopsis thaliana* homologue of PMS134 (AtPMS134) amino acid sequences. Similarity is 65.1%; identity is 50.7%. Black boxes show identical residues.



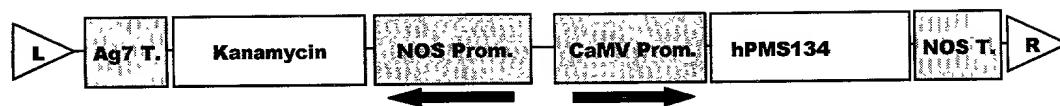
**Figure 8:** Western blot analysis of bacteria expressing the human PMS134 dominant negative gene (Panel A, lane 2) or the *Arabidopsis thaliana* dominant negative gene (Panel B, lane 2). Panel A, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the human PMS2 N-terminus. Panel B, lysates from bacteria were loaded onto SDS-PAGE gels and probed with an antibody against the flag epitope placed on the C-terminus of the *Arabidopsis* PMS134 gene. Lane 1 is bacteria containing empty vector as negative control



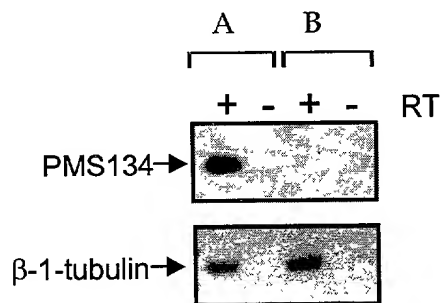
# Dominant Negative Effects of Arabidopsis thaliana PMS2 homolog



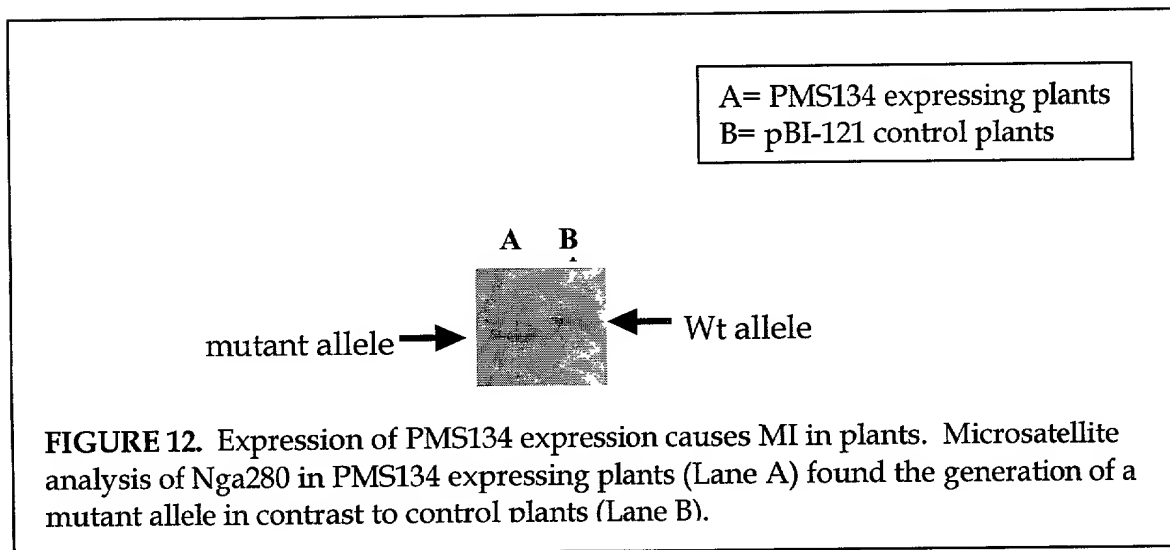
**Figure 9.** Expression of the *Arabidopsis thaliana* PMS134 gene produces hypermutability in bacteria leading to the generation of new phenotypes. Briefly, bacteria containing the empty vector or the TAC ATPMS134 expression vector were grown and plated on kanamycin containing Lbagar plates. The host bacteria are susceptible to KAN bactericidal activity. Bacterial cultures expressing the hPMS134 gene resulted in genetic alteration of the bacterial host and the generation of clones that are KAN resistant.



**Figure 10.** Schematic map of the pCMV-hPMS134-Kan binary plant expression vector. Ag7 T. and NOS T. = gene 7 and Nopaline Synthase poly(A) signals, respectively. NOS Prom and CaMV Prom = Nopaline Synthase and Cauliflower Mosaic Virus promoters, respectively. L and R = left and right T-DNA border repeats, respectively. Arrows indicate direction of transcription.



**Figure 11.** Expression of hPMS134 in *Arabidopsis Thailana*. Message analysis for T1 plants shows steady state expression of dominant negative MMR genes in PMS134-Kan plants (A) while none is observed in control plants (B). Tubulin was used as an internal control to monitor sample loading and integrity.



**Figure 13.** The plant on the left is a wild type *A. thaliana* and the one on the right is MMR defective. Seeds from the MMR defective plant have been obtained and offspring have the same “double-meristem” trait.

